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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/394,230	09/13/1999	KEVIN L. GUNDERSON	393382001600	3919

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SCHWEGMAN, LUNDBERG, WOESSNER & KLUTH, P.A.
P.O. BOX 2938
MINNEAPOLIS, MN 55402

EXAMINER	
FORMAN, BETTY J	

ART UNIT	PAPER NUMBER
1634	

DATE MAILED: 03/30/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/394,230	GUNDERSON ET AL.	
	Examiner	Art Unit	
	BJ Forman	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *18 January 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-10 and 12-18* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-10 and 12-18* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Continued Examination Under 37 CFR 1.114

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 18 January 2005 has been entered.

Status of the Claims

2. This action is in response to papers filed 18 January 2005 in which claims 11 and 19 were canceled. The amendments have been thoroughly reviewed and entered.

As stated in the Advisory Action of 9 December 2004, the previous objections to the specification and priority claim are withdrawn in view of the After-Final papers filed 22 November 2004. The previous rejection of Claims 1-10, 12-17 and 19 under 35 U.S.C. 102 (b) & (e) over Lockhart are withdrawn in view of the amended priority claim. The previous rejection of Claims 11 and 18 are maintained because the priority documents do not support the subject matter of these claim. The previous rejection of Claim 11 is withdrawn in view of the instant cancellation of the claim. All other rejections, not reiterated below, are withdrawn in view of the new grounds for rejection.

Applicant's arguments have been thoroughly reviewed but are deemed moot in view of the withdrawn rejections and new grounds for rejection. New grounds for rejection are discussed.

Claims 1-10, 12-18 are under prosecution.

Claim Rejections - 35 USC § 103

3. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

4. Claim 18 is rejected under 35 U.S.C. 103(a) as being unpatentable over Lockhart et al (WO/97,27317, published 31 July 1997) in view of Southern (U.S. Patent No. 5,700,637, filed 19 April 1994).

Regarding Claim 18, Lockhart et al disclose a method of determining the presence of a mutation in a target polynucleotide, comprising the steps of providing at least two identical polynucleotide probe arrays, each array comprising probes, wherein each probe comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each array constitute a complete set of n-mers (Fig. 13; page 71, lines 9-29 and page 74, lines 1-12) hybridizing the target polynucleotide to said overhangs of probe polynucleotides in one array to generate a target hybridization pattern hybridizing a reference polynucleotide to said overhangs of probe polynucleotides in a second array to generate a reference hybridization pattern and determining the presence of a mutation in the target polynucleotide by normalizing intensity differences of hybridized probes in the reference and target hybridization patterns comparing intensity differences of probes in the reference and target hybridization patterns and determining whether a mutation is present in the target polynucleotide (Example 20, pages 155-158) wherein the target-hybridized array and the reference-hybridized array are compared (page 156, line 29-page 157, line 7) which clearly suggests that the arrays are proximal to each other. But they do not specifically teach that the arrays are arranged in parallel.

However, Southern teaches the similar method wherein the arrays are arranged in parallel i.e. stripes (Column 7, lines 12-22) whereby numerous sequence variations are analyzed simultaneously wherein each stripe corresponds to a different sequence variation. It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to apply the parallel arrays (i.e. strips) of Southern for the array comparison of Lockhart et al for the expected benefit of analyzing numerous mutations simultaneously as taught by Southern (Column 7, lines 23-26).

5. Claims 1-10, 12-18 are rejected under 35 U.S.C. 103(a) as being unpatentable over Cantor et al. (U.S. Patent No. 5,631,134, filed 5 June 1995) in view of Rava et al (U.S. Patent No. 5,545,531, issued 13 August 1996).

Regarding Claim 1, Cantor et al. teach a method of determining the presence of a mutation in a target polynucleotide comprising the steps of providing a polynucleotide probe array wherein each probe comprises a double strand region and a single stranded n-mer overhang region; hybridizing a target polynucleotide to said overhangs in the array to generate a target hybridization pattern; and determining the presence of a mutation in the target polynucleotide by analyzing hybridization patterns (Column 8, lines 1-12) wherein the probes are designed to identify mutations (Column 4, lines 5-8) wherein the a single stranded n-mer overhang region is "preferably" about 4 to 20 nucleotides in length (Column 5, lines 60-65) and wherein the set of probes on the array comprises every possible n-mer (Column 6, lines 3-5). Cantor further provides two examples of complete n-mers (Example 1, Column 12, lines 9-19 & Example 2, Column 12, lines 57-67) wherein the array**s** made are characterized by comparative hybridization of known and unknown sequences (Column 13, lines 14-30). Furthermore, Cantor teaches their arrays are useful diagnostics for mutation identification (Column 4, lines

1-8) that clearly suggest comparative hybridization analysis because to determine a change in sequence (i.e. mutation) the sequence must be compared to an unchanged (wild-type) sequence. Absent the comparison, a mutation would not be recognized. Cantor et al do not specifically teach hybridization to two arrays and comparison and signal normalization to determine the presence of a mutation. However, it is noted that the instant specification (page 16) teaches this analysis was well known as taught by Rava et al.

Therefore, it would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to apply the well know two array-hybridization and signal comparison of Rava et al to the sequence analysis of Cantor based on Cantor's desire to analyze sequences to diagnose mutations (Column 4, lines 1-8).

Regarding Claim 2, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9).

Regarding Claim 3, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9). Cantor et al. do not discuss the reference polynucleotide. However, reference polynucleotides were known to one of ordinary skill in the art as discussed above and the skilled practitioner would have known that for comparison purposes, a target and reference polynucleotide would be treated equally i.e. ligated to the probe.

Regarding Claim 4, Cantor et al. teach the overhangs have free 5' ends (Column 12, lines 46-49 and Fig. 1B).

Regarding Claim 5, Cantor et al. teach the overhangs have free 3' ends (Column 12, lines 38-45 and Fig. 1A).

Regarding Claim 6, Cantor et al. teach the n-mer comprises from about 4 to 50 nucleotides (Column 12, lines 57-60).

Regarding Claims 7-9, Cantor et al. teach the mutation is a single nucleotide mutation (Column 10, lines 38-40). Cantor et al. do not teach the single nucleotide mutation is a substitution (Claim 7), a deletion (Claim 8) and an insertion (Claim 9). However, one skilled in

the art at the time the claimed invention was made would have known that the single nucleotide mutations taught by Cantor et al. include the claimed substitution, deletion and insertion mutations.

Regarding Claim 10, Cantor et al teach the method wherein single nucleotide mutations are identified wherein the identification quickly, efficiently and easily detects inherited mutations which cause disease and DNA depended phenotype and somatic variations (Column 10, lines 38-45). Cantor et al. do not teach the target polynucleotide is selected from the recited sequences. However, it would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to modify the method of Cantor et al. with the teachings of Cantor et al. to obtain the claimed invention because the skilled practitioner in the art would have been motivated with a reasonable expectation of success to apply the mutation detection teaching of Cantor et al. to sequences known to contain single nucleotide mutations for the obvious benefit of detecting clinically relevant mutations quickly, efficiently and easily as taught by Cantor et al.

Regarding Claim 12, Cantor et al. teach a method of determining relatedness two or more polynucleotides comprising the steps of providing a polynucleotide probe array wherein each probe comprises a double stranded region and a single stranded n-mer overhang region such that the over hangs in each array constitute a complete set of n-mers; hybridizing a target polynucleotide to said overhangs in the array to generate a hybridization pattern and analyzing the hybridization patterns (Column 8, lines 1-10) wherein the a single stranded n-mer overhang region is "preferably" about 4 to 20 nucleotides in length (Column 5, lines 60-65) and wherein the set of probes on the array comprises every possible n-mer (Column 6, lines 3-5).

Cantor further provides two examples of complete n-mers (Example 1, Column 12, lines 9-19 & Example 2, Column 12, lines 57-67) wherein the array**s** made are characterized by comparative hybridization of known and unknown sequences (Column 13, lines 14-30). Furthermore, Cantor teaches their arrays are useful diagnostics for mutation identification

(Column 4, lines 1-8) that clearly suggest comparative hybridization analysis because to determine a change in sequence (i.e. mutation) the sequence must be compared to an unchanged (wild-type) sequence. Absent the comparison, a mutation would not be recognized. Cantor et al do not specifically teach hybridization to two arrays and comparison and signal normalization to determine the presence of a mutation. However, it is noted that the instant specification (page 16) teaches this analysis was well known as taught by Rava et al.

Therefore, it would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to apply the well know two array-hybridization and signal comparison of Rava et al to the sequence analysis of Cantor based on Cantor's desire to analyze sequences to diagnose mutations (Column 4, lines 1-8)

Regarding Claim 13, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9).

Regarding Claim 14, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9). Cantor et al. do not discuss the reference polynucleotide. However, reference polynucleotides were known to one of ordinary skill in the art as discussed above and the skilled practitioner would have known that for comparison purposes, a target and reference polynucleotide would be treated equally i.e. ligated to the probe.

Regarding Claim 15, Cantor et al. teach the overhangs have free 5' ends (Column 12, lines 46-49 and Fig. 1B).

Regarding Claim 16, Cantor et al. teach the overhangs have free 3' ends (Column 12, lines 38-45 and Fig. 1A).

Regarding Claim 17, Cantor et al. teach the n-mer comprises from about 4 to 50 nucleotides (Column 12, lines 57-60).

Regarding Claim 18, Cantor et al. do not teach parallel arrays. However, Rava teaches parallel arrays (Fig.4).

6. Claims 1-10, 12-18 are rejected under 35 U.S.C. 103(a) as being unpatentable over Cantor et al. (U.S. Patent No. 5,631,134, filed 5 June 1995) in view of Brown et al (U.S. Patent No. 5,807,522, filed 7 June 1995) and Augenlicht (U.S. Patent No. 4,981,783, issued 1 January 1991).

Regarding Claim 1, Cantor et al. teach a method of determining the presence of a mutation in a target polynucleotide comprising the steps of providing a polynucleotide probe array wherein each probe comprises a double strand region and a single stranded n-mer overhang region; hybridizing a target polynucleotide to said overhangs in the array to generate a target hybridization pattern; and determining the presence of a mutation in the target polynucleotide by analyzing hybridization patterns (Column 8, lines 1-12) wherein the probes are designed to identify mutations (Column 4, lines 5-8) wherein the a single stranded n-mer overhang region is "preferably" about 4 to 20 nucleotides in length (Column 5, lines 60-65) and wherein the set of probes on the array comprises every possible n-mer (Column 6, lines 3-5). Cantor further provides two examples of complete n-mers (Example 1, Column 12, lines 9-19 & Example 2, Column 12, lines 57-67) wherein the array**s** made are characterized by comparative hybridization of known and unknown sequences (Column 13, lines 14-30). Furthermore, Cantor teaches their arrays are useful diagnostics for mutation identification (Column 4, lines 1-8), which clearly suggest comparative hybridization analysis because to determine a change in sequence (i.e. mutation) the sequence must be compared to an unchanged (wild-type) sequence. Absent the comparison, a mutation would not be recognized. Cantor et al do not specifically teach hybridization to two arrays and comparison and signal normalization to determine the presence of a mutation.

However, multi-array hybridization and analysis was well known in the art at the time the claimed invention was made as taught by Brown et al who teach that multi-array hybridization provides rapid and convenient mass screenings for diagnostic applications

(Column 15, lines 59-67). Furthermore, hybridization signal comparison and normalization was well known in the art as taught by Augenlicht who teach comparison and normalization of arrayed sequences for diagnosis and prognosis of disease (Abstract, and Column 4, lines 5-24 and 36-67).

It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to apply the well know multi-array hybridization and signal comparison of Brown et al and Augenlicht to the sequence analysis of Cantor for the expected benefit of rapid and convenient mass screenings for diagnostic and prognostic applications as taught by Brown et al (Column 15, lines 59-67) and Augenllicht (Abstract, and Column 4, lines 5-24 and 36-67).

Regarding Claim 2, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9).

Regarding Claim 3, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9). Cantor et al. do not discuss the reference polynucleotide. However, reference polynucleotides were known to one of ordinary skill in the art as discussed above and the skilled practitioner would have known that for comparison purposes, a target and reference polynucleotide would be treated equally i.e. ligated to the probe.

Regarding Claim 4, Cantor et al. teach the overhangs have free 5' ends (Column 12, lines 46-49 and Fig. 1B).

Regarding Claim 5, Cantor et al. teach the overhangs have free 3' ends (Column 12, lines 38-45 and Fig. 1A).

Regarding Claim 6, Cantor et al. teach the n-mer comprises from about 4 to 50 nucleotides (Column 12, lines 57-60).

Regarding Claims 7-9, Cantor et al. teach the mutation is a single nucleotide mutation (Column 10, lines 38-40). Cantor et al. do not teach the single nucleotide mutation is a substitution (Claim 7), a deletion (Claim 8) and an insertion (Claim 9). However, one skilled in the art at the time the claimed invention was made would have known that the single

nucleotide mutations taught by Cantor et al. include the claimed substitution, deletion and insertion mutations.

Regarding Claim 10, Cantor et al teach the method wherein single nucleotide mutations are identified wherein the identification quickly, efficiently and easily detects inherited mutations which cause disease and DNA depended phenotype and somatic variations (Column 10, lines 38-45). Cantor et al. do not teach the target polynucleotide is selected from the recited sequences. However, it would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to modify the method of Cantor et al. with the teachings of Cantor et al. to obtain the claimed invention because the skilled practitioner in the art would have been motivated with a reasonable expectation of success to apply the mutation detection teaching of Cantor et al. to sequences known to contain single nucleotide mutations for the obvious benefit of detecting clinically relevant mutations quickly, efficiently and easily as taught by Cantor et al.

Regarding Claim 12, Cantor et al. teach a method of determining relatedness two or more polynucleotides comprising the steps of providing a polynucleotide probe array wherein each probe comprises a double stranded region and a single stranded n-mer overhang region such that the over hangs in each array constitute a complete set of n-mers; hybridizing a target polynucleotide to said overhangs in the array to generate a hybridization pattern and analyzing the hybridization patterns (Column 8, lines 1-10) wherein the a single stranded n-mer overhang region is "preferably" about 4 to 20 nucleotides in length (Column 5, lines 60-65) and wherein the set of probes on the array comprises every possible n-mer (Column 6, lines 3-5).

Cantor further provides two examples of complete n-mers (Example 1, Column 12, lines 9-19 & Example 2, Column 12, lines 57-67) wherein the array**s** made are characterized by comparative hybridization of known and unknown sequences (Column 13, lines 14-30). Furthermore, Cantor teaches their arrays are useful diagnostics for mutation identification (Column 4, lines 1-8), which clearly suggest comparative hybridization analysis because to

determine a change in sequence (i.e. mutation) the sequence must be compared to an unchanged (wild-type) sequence. Absent the comparison, a mutation would not be recognized. Cantor et al do not specifically teach hybridization to two arrays and comparison and signal normalization to determine the presence of a mutation.

However, multi-array hybridization and analysis was well known in the art at the time the claimed invention was made as taught by Brown et al who teach that multi-array hybridization provides rapid and convenient mass screenings for diagnostic applications (Column 15, lines 59-67). Furthermore, hybridization signal comparison and normalization was well known in the art as taught by Augenlicht who teach comparison and normalization of arrayed sequences for diagnosis and prognosis of disease (Abstract, and Column 4, lines 5-24 and 36-67).

It would have been obvious to one of ordinary skill in the art at the time the claimed invention was made to apply the well know multi-array hybridization and signal comparison of Brown et al and Augenlicht to the sequence analysis of Cantor for the expected benefit of rapid and convenient mass screenings for diagnostic and prognostic applications as taught by Brown et al (Column 15, lines 59-67) and Augenllicht (Abstract, and Column 4, lines 5-24 and 36-67).

Regarding Claim 13, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9).

Regarding Claim 14, Cantor et al. teach the hybridized polynucleotide is ligated to the probe (Column 8, lines 8-9). Cantor et al. do not discuss the reference polynucleotide. However, reference polynucleotides were known to one of ordinary skill in the art as discussed above and the skilled practitioner would have known that for comparison purposes, a target and reference polynucleotide would be treated equally i.e. ligated to the probe.

Regarding Claim 15, Cantor et al. teach the overhangs have free 5' ends (Column 12, lines 46-49 and Fig. 1B).

Regarding Claim 16, Cantor et al. teach the overhangs have free 3' ends (Column 12, lines 38-45 and Fig. 1A).

Regarding Claim 17, Cantor et al. teach the n-mer comprises from about 4 to 50 nucleotides (Column 12, lines 57-60).

Regarding Claim 18, Cantor et al. do not teach parallel arrays. However, Brown et al (Fig. 9) and Augenlicht (Fig. 1) teach parallel arrays.

Double Patenting

7. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

8. Claims 1-10, 12-28 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-4 and 18 of U.S. Patent No. 6,344,316. Although the conflicting claims are not identical, they are not patentably distinct from each other because both sets of claims are drawn to methods of polynucleotide analysis comprising the same steps of hybridizing polynucleotides from two samples to probe arrays and determining a different in hybridization to analyze the polynucleotide wherein the probes of the arrays comprise double-stranded regions and single-stranded regions. The claim sets merely differ in the arrangement of the limitations within the claim sets and the intended use

of the method steps. For example, the instant claims are drawn to determining the presence of a mutation and whether the polynucleotides are identical while the '316 claims are drawn to identifying differences. However, because both sets of claims contain the same method steps, the intended use for the methods does not patentably distinguish the two claim sets. Furthermore, the instant independent claims define the probes as comprising double-stranded regions and single-stranded regions while dependent Claim 18 provides the same definition of the probes. As such, the claim sets are drawn to methods that are not patentably distinct from each other.

Conclusion

9. No claim is allowed.

10. Any inquiry concerning this communication or earlier communications from the examiner should be directed to BJ Forman whose telephone number is (571) 272-0741. The examiner can normally be reached on 6:00 TO 3:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones can be reached on (571) 272-0745. The fax phone number for the organization where this application or proceeding is assigned is (571) 273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your

application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

BJ Forman, Ph.D.
Primary Examiner
Art Unit: 1634
March 24, 2005